Name _____ **Period** _____

Ms. Foglia **Date** _____

AP: CHAPTER 20: DNA TECHNOLOGY

1. Define biotechnology.

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2. What is meant by “recombinant DNA technology?”

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3. List some of the organisms we have been modifying for many hundreds of years.

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4. Why are bacteria ideal workhorses for biotechnology?

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5. What are other organisms used in biotechnology?

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6. How does gene cloning differ from human cloning?

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2004-2005

7. Why is DNA cloning considered an important technology?

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8. What are plasmids?

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9. What is the function of restriction enzymes in bacteria?

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10. How do bacteria protect their DNA from the effects of the restriction enzymes?

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11. How do biologists make use of restriction enzymes?

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12. What is a genomic library?

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13. How is cDNA different from typical eukaryote DNA?

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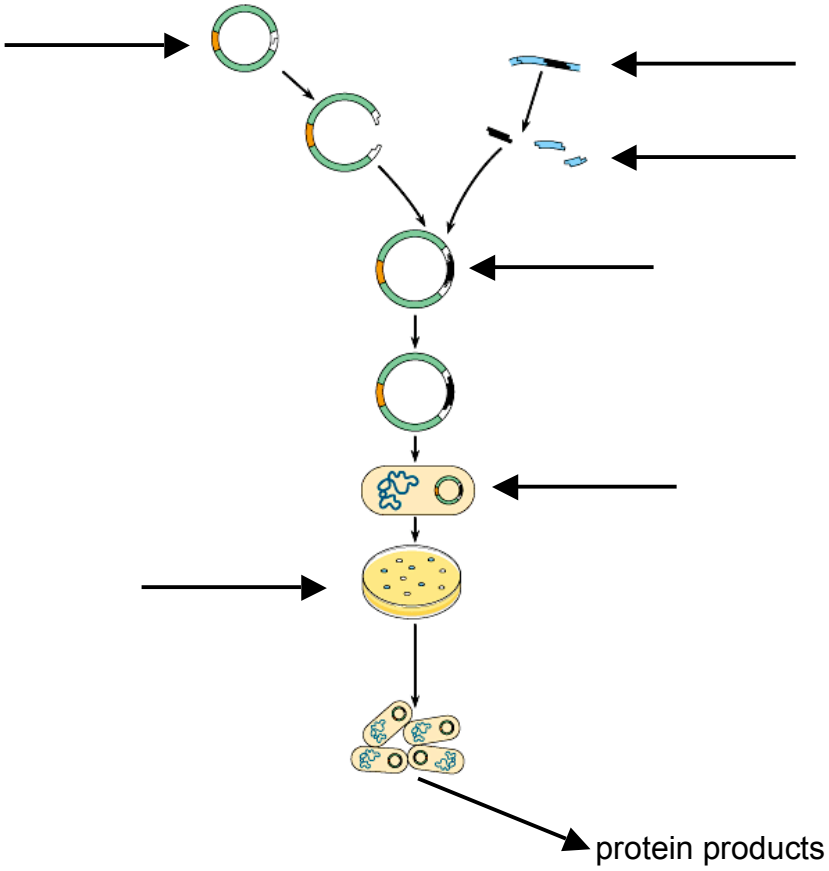
14. Describe the steps involved in cloning a gene.



15. How can transformed bacteria that carry genes of interest be identified and isolated from the majority of non-transformed bacteria?

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16. What can be accomplished with Nucleic Acid Hybridization?

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17. What is the purpose of the Polymerase Chain Reaction?

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18. List some advantages & uses of the PCR technique.

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19. How are DNA fragments of different sizes separated?

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20. What is a RFLP? How are they made?

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21. What does the technique of Southern Blotting accomplish?

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22. What are some other techniques that build on the Southern Blotting technique?

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23. What was the goal of the Human Genome Project?

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24. List some of the most important things we learned by completing the Human Genome Project.

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25. What is the Sanger Sequencing Method used for?

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26. How does the shot-gun approach differ from the whole-genome sequencing?

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27. In the future, DNA chips may be used for regular diagnostics. What do the florescent spots indicate when the chip is read?

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28. How can DNA technology be used to diagnose a carrier of a genetic disorder?

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29. What is the goal of gene therapy?

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30. How has forensics made use of DNA technology? Give a specific example.

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31. What is currently used by the FBI to do a DNA fingerprint in a criminal investigation?

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32. What technique has been used to modify agricultural plants?

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33. List a few of the traits that have been engineered into agricultural plants? Could any of these pose an environmental threat?

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INSIGHTS LEARNED FROM THE SEQUENCE

What has been learned from analysis of the working draft sequence of the human genome? What is still unknown?*

*information taken from Science, Nature, Wellcome Trust, and Human Genome News

By the Numbers

- The human genome contains 3164.7 million chemical nucleotide bases (A, C, T, and G).
- The average gene consists of 3000 bases, but sizes vary greatly, with the largest known human gene being dystrophin at 2.4 million bases.
- The total number of genes is estimated at 30,000 to 35,000, much lower than previous estimates of 80,000 to 140,000 that had been based on extrapolations from gene-rich areas as opposed to a composite of gene-rich and gene-poor areas.
- The order of almost all (99.9%) nucleotide bases are exactly the same in all people.
- The functions are unknown for over 50% of discovered genes.

The Wheat from the Chaff

- Less than 2% of the genome encodes for the production of proteins.
- Repeated sequences that do not code for proteins ("junk DNA") make up at least 50% of the human genome.
- Repetitive sequences are thought to have no direct functions, but they shed light on chromosome structure and dynamics. Over time, these repeats reshape the genome by rearranging it, thereby creating entirely new genes or modifying and reshuffling existing genes.
- During the past 50 million years, a dramatic decrease seems to have occurred in the rate of accumulation of repeats in the human genome.

How It's Arranged

- The human genome's gene-dense "urban centers" are predominantly composed of the DNA building blocks G and C.
- In contrast, the gene-poor "deserts" are rich in the DNA building blocks A and T. GC- and AT-rich regions usually can be seen through a microscope as light and dark bands on chromosomes.
- Genes appear to be concentrated in random areas along the genome, with vast expanses of noncoding DNA between.
- Stretches of up to 30,000 C and G bases repeating over and over often occur adjacent to gene-rich areas, forming a barrier between the genes and the "junk DNA." These CpG islands are believed to help regulate gene activity.

- Chromosome 1 has the most genes (2968), and the Y chromosome has the fewest (231).

How the Human Genome Compares with That of Other Organisms

- Unlike the human's seemingly random distribution of gene-rich areas, many other organisms' genomes are more uniform, with genes evenly spaced throughout.
- Humans have on average three times as many kinds of proteins as the fly or worm because of mRNA transcript "alternative splicing" and chemical modifications to the proteins. This process can yield different protein products from the same gene.
- Humans share most of the same protein families with worms, flies, and plants, but the number of gene family members has expanded in humans, especially in proteins involved in development and immunity.
- The human genome has a much greater portion (50%) of repeat sequences than the mustard weed (11%), the worm (7%), and the fly (3%).
- Although humans appear to have stopped accumulating repeated DNA over 50 million years ago, there seems to be no such decline in rodents. This may account for some of the fundamental differences between hominids and rodents, although gene estimates are similar in these species. Scientists have proposed many theories to explain evolutionary contrasts between humans and other organisms, including those of life span, litter sizes, inbreeding, and genetic drift.

Variations and Mutations

- Scientists have identified about 1.4 million locations where single-base DNA differences (SNPs) occur in humans. This information promises to revolutionize the processes of finding chromosomal locations for disease-associated sequences and tracing human history.
- The ratio of germline (sperm or egg cell) mutations is 2:1 in males vs females. Researchers point to several reasons for the higher mutation rate in the male germline, including the greater number of cell divisions required for sperm formation than for eggs.

What We Still Don't Know: A Checklist for Future Research

- Exact gene number, exact locations, and functions
- Gene regulation
- DNA sequence organization
- Chromosomal structure and organization
- Noncoding DNA types, amount, distribution, information content, and functions
- Coordination of gene expression, protein synthesis, and post-translational events
- Interaction of proteins in complex molecular machines
- Predicted vs experimentally determined gene function
- Evolutionary conservation among organisms
- Protein conservation (structure and function)

- Proteomes (total protein content and function) in organisms
- Correlation of SNPs (single-base DNA variations among individuals) with health and disease
- Disease-susceptibility prediction based on gene sequence variation
- Genes involved in complex traits and multigene diseases
- Complex systems biology, including microbial consortia useful for environmental restoration
- Developmental genetics, genomics

http://genome.gsc.riken.go.jp/hgmis/project/journals/insights.html